

SEQUENCE LISTING



#12/B

<110> CLAUSEN, Henrik

<120> UDP-N-ACETYLGLUCOSAMINE: GALACTOSE-B1, 3-N-ACETYLGLACTOSAMINE-a-R / N-ACETYL GLUCOSAMINE-B1,3-N-ACETYLGLACTOSAMINE-a-R (GlcNAc to GalNAc) B1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE, C2/4GnT

<130> 4305/0J425

<140> US 09/874,390

<141> 2001-06-04

<150> DK PA 1988 01605

<151> 1998-12-04

<160> 12

<170> PatentIn version 3.1

<210> 1

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<212> DNA

<213> Homo sapiens

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accttttgga gggtagaag atcaggggac atgggtgttc acatttgctg ccacggaaca	360
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Leu Trp Ala Leu Gly Cys Tyr Met Leu Leu Ala Thr Val Ala Leu Lys	
15 20 25	
ctt tct ttc agg ttg aag tgt gac tct gac cac ttg ggt ctg gag tcc	627
Leu Ser Phe Arg Leu Lys Cys Asp Ser Asp His Leu Gly Leu Glu Ser	

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Leu Lys Cys Asp Ser Asp His Leu Gly Leu Glu Ser Arg Glu Ser Gln  
 35 40 45

Ser Gln Tyr Cys Arg Asn Ile Leu Tyr Asn Phe Leu Lys Leu Pro Ala  
 50 55 60

Lys Arg Ser Ile Asn Cys Ser Gly Val Thr Arg Gly Asp Gln Glu Ala  
 65 70 75 80

Val Leu Gln Ala Ile Leu Asn Asn Leu Glu Val Lys Lys Lys Arg Glu  
 85 90 95

Pro Phe Thr Asp Thr His Tyr Leu Ser Leu Thr Arg Asp Cys Glu His  
 100 105 110

Phe Lys Ala Glu Arg Lys Phe Ile Gln Phe Pro Leu Ser Lys Glu Glu  
 115 120 125

Val Glu Phe Pro Ile Ala Tyr Ser Met Val Ile His Glu Lys Ile Glu  
 130 135 140

Asn Phe Glu Arg Leu Leu Arg Ala Val Tyr Ala Pro Gln Asn Ile Tyr  
 145 150 155 160

Cys Val His Val Asp Glu Lys Ser Pro Glu Thr Phe Lys Glu Ala Val  
 165 170 175

Lys Ala Ile Ile Ser Cys Phe Pro Asn Val Phe Ile Ala Ser Lys Leu  
180 185 190

Val Arg Val Val Tyr Ala Ser Trp Ser Arg Val Gln Ala Asp Leu Asn  
195 200 205

Cys Met Glu Asp Leu Leu Gln Ser Ser Val Pro Trp Lys Tyr Phe Leu  
210 215 220

Asn Thr Cys Gly Thr Asp Phe Pro Ile Lys Ser Asn Ala Glu Met Val  
225 230 235 240

Gln Ala Leu Lys Met Leu Asn Gly Arg Asn Ser Met Glu Ser Glu Val  
245 250 255

Pro Pro Lys His Lys Glu Thr Arg Trp Lys Tyr His Phe Glu Val Val  
260 265 270

Arg Asp Thr Leu His Leu Thr Asn Lys Lys Lys Asp Pro Pro Pro Tyr  
275 280 285

Asn Leu Thr Met Phe Thr Gly Asn Ala Tyr Ile Val Ala Ser Arg Asp  
290 295 300

Phe Val Gln His Val Leu Lys Asn Pro Lys Ser Gln Gln Leu Ile Glu  
305 310 315 320

Trp Val Lys Asp Thr Tyr Ser Pro Asp Glu His Leu Trp Ala Thr Leu  
325 330 335

Gln Arg Ala Arg Trp Met Pro Gly Ser Val Pro Asn His Pro Lys Tyr  
340 345 350

Asp Ile Ser Asp Met Thr Ser Ile Ala Arg Leu Val Lys Trp Gln Gly  
355 360 365

His Glu Gly Asp Ile Asp Lys Gly Ala Pro Tyr Ala Pro Cys Ser Gly  
370 375 380

Ile His Gln Arg Ala Ile Cys Val Tyr Gly Ala Gly Asp Leu Asn Trp  
385 390 395 400

Met Leu Gln Asn His His Leu Leu Ala Asn Lys Phe Asp Pro Lys Val  
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Asp Asp Asn Ala Leu Gln Cys Leu Glu Glu Tyr Leu Arg Tyr Lys Ala  
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Ile Tyr Gly Thr Glu Leu  
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26

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Arg Ile His Gln Lys Pro Glu Phe Val Ser Val Arg His Leu Glu Leu  
35 40 45

Ala Gly Glu Asn Pro Ser Ser Asp Ile Asn Cys Thr Lys Val Leu Gln  
50 55 60

Gly Asp Val Asn Glu Ile Gln Lys Val Lys Leu Glu Ile Leu Thr Val  
65 70 75 80

Lys Phe Lys Lys Arg Pro Arg Trp Thr Pro Asp Asp Tyr Ile Asn Met  
85 90 95

Thr Ser Asp Cys Ser Ser Phe Ile Lys Arg Arg Lys Tyr Ile Val Glu  
100 105 110

Pro Leu Ser Lys Glu Glu Ala Glu Phe Pro Ile Ala Tyr Ser Ile Val  
115 120 125

Val His His Lys Ile Glu Met Leu Asp Arg Leu Leu Arg Ala Ile Tyr  
130 135 140

Met Pro Gln Asn Phe Tyr Cys Val His Val Asp Thr Lys Ser Glu Asp  
145 150 155 160

Ser Tyr Leu Ala Ala Val Met Gly Ile Ala Ser Cys Phe Ser Asn Val  
165 170 175

Phe Val Ala Ser Arg Leu Glu Ser Val Val Tyr Ala Ser Trp Ser Arg  
180 185 190

Val Gln Ala Asp Leu Asn Cys Met Lys Asp Leu Tyr Ala Met Ser Ala  
195 200 205

Asn Trp Lys Tyr Leu Ile Asn Leu Cys Gly Met Asp Phe Pro Ile Lys  
210 215 220



Thr Asn Leu Glu Ile Val Arg Lys Leu Lys Leu Leu Met Gly Glu Asn  
225 230 235 240

Asn Leu Glu Thr Glu Arg Met Pro Ser His Lys Glu Glu Arg Trp Lys  
245 250 255

Lys Arg Tyr Glu Val Val Asn Gly Lys Leu Thr Asn Thr Gly Thr Val  
260 265 270

Lys Met Leu Pro Pro Leu Glu Thr Pro Leu Phe Ser Gly Ser Ala Tyr  
275 280 285

Phe Val Val Ser Arg Glu Tyr Val Gly Tyr Val Leu Gln Asn Glu Lys  
290 295 300

Ile Gln Lys Leu Met Glu Trp Ala Gln Asp Thr Tyr Ser Pro Asp Glu  
305 310 315 320

Tyr Leu Trp Ala Thr Ile Gln Arg Ile Pro Glu Val Pro Gly Ser Leu  
325 330 335

Pro Ala Ser His Lys Tyr Asp Leu Ser Asp Met Gln Ala Val Ala Arg  
340 345 350

Phe Val Lys Trp Gln Tyr Phe Glu Gly Asp Val Ser Lys Gly Ala Pro  
355 360 365

Tyr Pro Pro Cys Asp Gly Val His Val Arg Ser Val Cys Ile Phe Gly  
370 375 380

Ala Gly Asp Leu Asn Trp Met Leu Arg Lys His His Leu Phe Ala Asn  
385 390 395 400

Lys Phe Asp Val Asp Val Asp Leu Phe Ala Ile Gln Cys Leu Asp Glu  
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His Leu Arg His Lys Ala Leu Glu Thr Leu Lys His  
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Phe Gln Arg Leu Asn Ile Ser Asp Pro Leu Arg Leu Thr Gln Val Cys  
35 40 45

Thr Ser Phe Ile Asn Gly Lys Thr Arg Phe Leu Trp Lys Asn Lys Leu  
50 55 60

Met Ile His Glu Lys Ser Ser Cys Lys Glu Tyr Leu Thr Gln Ser His  
65 70 75 80

Tyr Ile Thr Ala Pro Leu Ser Lys Glu Glu Ala Asp Phe Pro Leu Ala  
85 90 95

Tyr Ile Met Val Ile His His His Phe Asp Thr Phe Ala Arg Leu Phe  
100 105 110

Arg Ala Ile Tyr Met Pro Gln Asn Ile Tyr Cys Val His Val Asp Glu  
115 120 125

Lys Ala Thr Thr Glu Phe Lys Asp Ala Val Glu Gln Leu Leu Ser Cys  
130 135 140

Phe Pro Asn Ala Phe Leu Ala Ser Lys Met Glu Pro Val Val Tyr Gly  
145 150 155 160

Gly Ile Ser Arg Leu Gln Ala Asp Leu Asn Cys Ile Arg Asp Leu Ser  
165 170 175

Ala Phe Glu Val Ser Trp Lys Tyr Val Ile Asn Thr Cys Gly Gln Asp  
180 185 190

Phe Pro Leu Lys Thr Asn Lys Glu Leu Val Gln Tyr Leu Lys Gly Phe  
195 200 205

Lys Gly Lys Asn Ile Thr Pro Gly Val Leu Pro Pro Ala His Ala Ile  
210 215 220

Gly Arg Thr Lys Tyr Val His Gln Glu His Leu Gly Lys Glu Leu Ser  
225 230 235 240

Tyr Val Ile Arg Thr Thr Ala Leu Lys Pro Pro Pro Pro His Asn Leu  
245 250 255

Thr Ile Tyr Phe Gly Ser Ala Tyr Val Ala Leu Ser Arg Glu Phe Ala  
260 265 270

Asn Phe Val Leu His Asp Pro Arg Ala Val Asp Leu Leu Gln Trp Ser  
275 280 285

Lys Asp Thr Phe Ser Pro Asp Glu His Phe Trp Val Thr Leu Asn Arg  
290 295 300

Ile Pro Gly Val Pro Gly Ser Met Pro Asn Ala Ser Trp Thr Gly Asn  
305 310 315 320

Leu Arg Ala Ile Lys Trp Ser Asp Met Glu Asp Arg His Gly Gly Cys  
325 330 335

His Gly His Tyr Val His Gly Ile Cys Ile Tyr Gly Asn Gly Asp Leu  
340 345 350

Lys Trp Leu Val Asn Ser Pro Ser Leu Phe Ala Asn Lys Phe Glu Leu  
355 360 365

Asn Thr Tyr Pro Leu Thr Val Glu Cys Leu Glu Leu Arg His Arg Glu  
370 375 380

Arg Thr Leu Asn Gln Ser Glu Thr Ala Ile Gln Pro Ser Trp Tyr Phe  
385 390 395 400